Package 'sCPUEdb'

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Title The Shark CPUE Database

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Description Package to explore and use the shark CPUE database. The shark CPUE database is a compilation of shark indices of abundance from all over the world.

Depends R (>= 3.1.2)

License GPL-2

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

Imports maps, maptools, raster, fields, mapdata, dplyr, plyr, RColorBrewer, sp

R topics documented:

`connectPelagic` *Create Connection to Pelagic Database on Baseline3.*

Description

Create Connection to Pelagic Database on Baseline3. This connection grant permission to select on tables: master, timseries, iccatt2ce, iotccell, wcpfc, iattc.

Usage

```
connectPelagic(dbuser = "rpackage", dbpass = "sCPUEdb")
```

Arguments

`dbuser`	role name for database
`dbpass`	database password for role ‘dbuser‘

`convertClasses` *Convert classes of a data.frame columns to specified kind*

Description

Convert classes of a data.frame columns to specified kind

Usage

```
convertClasses(df, classes)
```

Arguments

`df`	data.frame
`classes`	vector of classes

coord2grid *Convert Database Polygon (coord) to SpatialGridDataFrame*

Description

This function takes a 'coord' string, a spatial polygon that identify a time series of data and convert it to SpatialGridDataFrame of a certain resolution (default is 5 degrees of resolution)

Usage

```
coord2grid(coord, Reslon = 5, Reslat = 5)
```

Arguments

coord	a string identifying a spatial polygon in the sCPUE database
Reslon	longitudinal resolution
Reslat	latitudinal resolution

coord2polygon *Generate R polygons from coord in the pelagic database*

Description

Generate R polygons from coord in the pelagic database

Usage

```
coord2polygon(coord)
```

Arguments

coord	vector of coords

Value

an R polygon

csv2table *Send csv to Database Table*

Description

The function it is used to substitute chunks of Timeseries and Master. It takes the temTable.csv in the working directory (obtained through `table2csv`) and submit it to the database into the target table and for reference ref

Usage

```
csv2table(con, file = "temTable.csv", ref, Table = "master")
```

Arguments

`con`	connection to db
`ref`	ref code
`Table`	target table

expandRMFO *expand RMFO dataset to full resolution*

Description

It expands all catches to 1 degree cell in latitude and longitude. It takes a pixel of any size in degres and expand the correspondent row in dat to a number of rows equal to the number of 1 degree pixels contained in this larger pixel identified by res

Usage

```
expandRMFO(dat)
```

Arguments

`dat`	a dataset with a res (resolution, e.g. 5*5) field. dat should have a lat and lon field too.

expandRMFO2 *expand RMFO dataset to full resolution*

Description

It expands all catches to Reslat by Reslon degree cell in latitude and longitude. It takes a pixel of any size in degrees and expand the correspondent row in 'dat' to a number of rows equal to the number of Reslat degree pixels contained in this larger pixel identified by dat$res

Usage

```
expandRMFO2(dat, Reslat, Reslon)
```

Arguments

dat	a dataset with a res (resolution, e.g. 5*5) field. dat should have a lat and lon field too. param Reslat terget resolution for the expanded dataset param Reslon target resolution for the expanded dataset. It works if Reslat = Reslon

extractBib *extract reference list from db*

Description

script to update the reference list in the website from the database

Usage

```
extractBib(con, conditions = "where species = 'Prionace glauca'",
  fileName = "pelagicRefs")
```

Arguments

con	connection handle
conditions	specify where clause on the master table selecting for distinct refs
fileName	name of the output file without extension

Value

it will output a bib and tex file with file name. A problem with this function is that it does not returns the list of references missing in the aic master bib file.

getGlobalEffort *Build all the effort data. Resolution is 5 degrees.*

Description

Build all the effort data. Resolution is 5 degrees.

Usage

```
getGlobalEffort(con, Reslat = 1, Reslon = 1, fullres = FALSE)
```

Arguments

con	a connection to the 'sCPUEdb'
Reslat	latitudinal resolution.
Reslon	longitudinal resolution.
fullres	I want the dataset at full resolution - so all resolutions. This aspect pertains to IOTC and ICCAT data

getIATTCdata *get IATTC longline data from local file*

Description

This csv file needs to be included in the database. The data is only for longline. Need to produce a similar function for purse seine.

Usage

```
getIATTCdata(con, bbox = NULL)
```

Arguments

con	a connection to the sCPUEdb
bbox	bounding box. It can be c(minlat,maxlat,minlon,maxlon) or NULL

Value

lat and lon refer to the SW corner of pixel

getIATTCdataCE *get IATTC longline Catch and Effort data for a certain species*

Description

This csv file needs to be included in the database. The data is only for longline. Need to produce a similar function for purse seine.

Usage

```
getIATTCdataCE(con, code = "alb", index = "n")
```

Arguments

con	a connection to the sCPUEdb
code	IATTC species code. It can be "alb", "bet", "pbf", "skj", "tun", "yft", "bil", "blm", "bum", "mls", "sfa", "ssp", "swo".
index	can be 'n' for numbers and 'mt' for biomass
bbox	bounding box. It can be c(minlat,maxlat,minlon,maxlon) or NULL

Value

lat and lon refer to the SW corner of pixel

getICCATdata *get catch and effort data from ICCAT*

Description

get ICCAT longline effort data from the task II catch and effort database. June 30, 2016 at 8:49:27 AM PDT finish to fix the function with new database schema

Usage

```
getICCATdata(con, Reslat = 5, Reslon = 5, fullres = FALSE)
```

Arguments

con	a connection to the sCPUEdb
Reslat	latitudinal resolution. It is used only when fullres = FALSE. Else the resolutions are all different
Reslon	longitudinal resolution
fullres	if TRUE it gets data in all resolutions as they were included. So Reslat and Reslon are no more relevant.

Value

each pixel is marked at its SW corner

getICCATdataCPUE *get CPUE data*

Description

get CPUE data at 5x5 resolution. I am going to modify this for all resolutions

Usage

```
getICCATdataCPUE(catch = "BSH", effort = "Eff1", CatchUnit = "nr",
  fleetID = "all")
```

getIOTCdata *get Indian Ocean Tuna Commission catch and effort data*

Description

get Indian Ocean Tuna Commission catch and effort data

Usage

```
getIOTCdata(con, Reslat = 5, Reslon = 5, fullres = FALSE)
```

Arguments

con	connection to the sCPUEdb
Reslat	latitude resolution
Reslon	longitude resolution
fullres	if TRUE return full resolution data. That means it returns the data in all resolutions as they were submitted.

Value

a data.frame with ‘lat‘, ‘lon‘, ‘year‘, ‘hooks‘ and ‘fleet‘; lat and lon refer to the SW corner of pixel.

getIOTCdataCE *get Indian Ocean Tuna Commission Catch and Effort data*

Description

get Indian Ocean Tuna Commission Catch and Effort data

Usage

```
getIOTCdataCE(con, catch = "bsh_no")
```

Arguments

con	connection to the sCPUEdb
catch	species to extract

Value

a data.frame with ‘lat‘, ‘lon‘, ‘year‘, ‘hooks‘ and ‘fleet‘; lat and lon refer to the SW corner of pixel.

getMaterial *extract the name of the table or figure*

Description

it is use by ExtractCatches

Usage

```
getMaterial(cell)
```

Arguments

cell	text tring containing the figure/table names

`getNEmptyCol` *Returns a table from any table in the pelagic DB with non-empty columns.*

Description

Returns a table from any table in the pelagic DB with non-empty columns.

Usage

```
getNEmptyCol(con, ref, Table = "master")
```

Arguments

`con`	connection to the database
`ref`	refcode of the data
`Table`	table name of the shark CPUE database

`getNEmptyCol2` *'getNEmptyCol' with the option to specify the where clause*

Description

'getNEmptyCol' with the option to specify the where clause

Usage

```
getNEmptyCol2(con, ref, Table = "master", where = "")
```

`getNumberSpecies` *Get the number of species from the database.*

Description

The function extracts the data from the master table and excludes all entries not having a binomial scientific name.

Usage

```
getNumberSpecies(con)
```

Arguments

`con`	a connection to the sCPUEdb

getSpecies *get all the species available in the shark CPUE db*

Description

get all the species available in the shark CPUE db

Usage

```
getSpecies(con)
```

Arguments

con	a connection to teh database. It shoud be run after 'connectPelagic'.

getTable *get a table from the baseline2 machine not from the database*

Description

it reads the source files of the database. So it check whether the data has been inputted, in that case the table is in the 'data' folder, else it checks into the 'datainDB' folder. This is useful to have a more synthetic view of the data populating the tables in the database. They do not include column with missing values.

Usage

```
getTable(Table = "Master", address = "data/", ref, inDB = FALSE)
```

Arguments

Table	is the table file to extract from the server
address	location of the data
ref	refcode of the data to explore
inDB	whether the data files have been included in the postgresql database. If the function fails try this option.

getUnit *extract unit from celles with data addresses (e.g. Tab1[,2])*

Description

extract unit from celles with data addresses (e.g. Tab1[,2])

Usage

```
getUnit(cell)
```

Arguments

cell	text content of the cell - characteri string

getWCPFCdata *get WCPFC data from connection*

Description

get WCPFC data from connection

Usage

```
getWCPFCdata(con)
```

Arguments

con	connection to the pelagic database

Value

data.frame with lat, lon, year and hooks. It refer to all fleets fishing in the area. ‘Lat‘ and ‘lon‘ refer to the SW corner of pixel.

getWCPFCdataCE *get WCPFC Catch and Effort data from connection*

Description

get WCPFC Catch and Effort data from connection

Usage

```
getWCPFCdataCE(con, code = "yft", index = "n")
```

Arguments

con	connection to the pelagic database
code	WCPFC species code. Possible values are "alb" "yft" "bet" "mls" "blm" "bum" "swo" "oth"
index	it can be either "n" (for numbers) or "c" (for metric tonnes).

Value

data.frame with lat, lon, year and hooks. It refer to all fleets fishing in the area. ‘Lat‘ and ‘lon‘ refer to the SW corner of pixel.

mapAreas *Map all areas in the database.*

Description

The function builds a multipage pdf that shows all the areas in the sCPUEdb (one polygon and map per page).

Usage

```
mapAreas(con)
```

Arguments

con	a pelagic database connection

mapAreasTogether *Map all Polygons Together*

Description

All polygons drawn together on a global map

Usage

```
mapAreasTogether(con, refs = NULL)
```

Arguments

con	connection to database
refs	list of studies to plot given by a vector of reference codes.

mapAreasTRef *Map all polygons pertaining to a single ref*

Description

Map all polygons pertaining to a single ref

Usage

```
mapAreasTRef(con, ref)
```

Arguments

con	connection object
ref	reference code

mapAreasTSpecies *Map all areas (polygons) of a given species*

Description

Map all areas (polygons) of a given species

Usage

```
mapAreasTSpecies(con, species)
```

Arguments

con	connection object
species	species name

openPdf *open the pdf file related to ref*

Description

open the pdf file related to ref

Usage

```
openPdf(ref)
```

Arguments

ref	code for the publication

plotCPUE *Plot CPUEs for a given species*

Description

Plot CPUEs for a given species

Usage

```
plotCPUE(species = "Prionace glauca", region = "Indian", index = "scpue",
  dat = NULL)
```

Arguments

species	species names
region	large oceanic region as codified in regions table. It could be a part of the entire name as it will be used in the clause like '%",region,"%'
index	index of abundance to plot
dat	optional is the supplied dataset from an external query

searchDatasets *Search Data Sets*

Description

the function searches the datasets identified by geographic polygons in the database.

Usage

```
searchDatasets(searchBox = "((-176.57,11.87),(-176.57,29.99),(-135.88,29.99),(-135.88,11.87))")
```

Arguments

searchBox	a search box in the coord format. Default searches studies around Hawaii. "((-176.57,11.87),(-176.57,29.99),(-135.88,29.99),(-135.88,11.87))"

Value

a list of refs that can be included in another function.

table2csv *Extract values from database table and put them into a csv file*

Description

This function is used to edit chunks of database tables

Usage

```
table2csv(con, query, file = "temTable.csv", openfile = TRUE)
```

Arguments

con	database connection
query	the psql query to use
file	csv file to output

Index